What is claimed is:

1.   A polypeptide chain useful as a subunit of a
dimeric osteogenic protein comprising a pair of
disulfide-bonded polypeptide chains,
        said polypeptide chain having an amino acid
sequence sufficiently duplicative of Sequence ID No.
1 or Sequence ID No. 3 such that the dimeric
osteogenic protein comprising said polypeptide chain
has a conformation capable of inducing endochondral
bone formation when implanted in a mammal in
association with a matrix.

2.   The polypeptide chain of claim 1 wherein the
sequence comprises (Sequence ID No. 1):

<u>mOP-2</u>

Ala 1	Ala	Arg	Pro	Leu 5	Lys	Arg	Arg	Gln
Pro 10	Lys	Lys	Thr	Asn	Glu 15	Leu	Pro	His
Pro	Asn 20	Lys	Leu	Pro	Gly	Ile 25	Phe	Asp
Asp	Gly	His 30	Gly	Ser	Arg	Gly	Arg 35	Glu
Val	Cys	Arg	Arg 40	His	Glu	Leu	Tyr	Val 45
Arg	Phe	Arg	Asp	Leu 50	Gly	Trp	Leu	Asp
Trp 55	Val	Ile	Ala	Pro	Gln 60	Gly	Tyr	Ser

```
Ala   Tyr   Tyr   Cys   Glu   Gly   Glu   Cys   Ala
      65                            70

Phe   Pro   Leu   Asp   Ser   Cys   Met   Asn   Ala
            75                            80

Thr   Asn   His   Ala   Ile   Leu   Gln   Ser   Leu
                  85                            90

Val   His   Leu   Met   Lys   Pro   Asp   Val   Val
                        95

Pro   Lys   Ala   Cys   Cys   Ala   Pro   Thr   Lys
100                           105

Leu   Ser   Ala   Thr   Ser   Val   Leu   Tyr   Tyr
      110                           115

Asp   Ser   Ser   Asn   Asn   Val   Ile   Leu   Arg
            120                           125

Lys   His   Arg   Asn   Met   Val   Val   Lys   Ala
                  130                           135

Cys   Gly   Cys   His.
```

3.   The polypeptide chain of claim 1 wherein the
sequence comprises (Sequence ID No. 3):

<u>hOP-2</u>

```
Ala   Val   Arg   Pro   Leu   Arg   Arg   Arg   Gln
1                       5

Pro   Lys   Lys   Ser   Asn   Glu   Leu   Pro   Gln
10                            15

Ala   Asn   Arg   Leu   Pro   Gly   Ile   Phe   Asp
      20                            25

Asp   Val   Asn   Gly   Ser   His   Gly   Arg   Gln
            30                            35

Val   Cys   Arg   Arg   His   Glu   Leu   Tyr   Val
                  40                            45
```

```
Ser   Phe   Gln   Asp   Leu   Gly   Trp   Leu   Asp
                        50

Trp   Val   Ile   Ala   Pro   Gln   Gly   Tyr   Ser
55                            60

Ala   Tyr   Tyr   Cys   Glu   Gly   Glu   Cys   Ser
      65                            70

Phe   Pro   Leu   Asp   Ser   Cys   Met   Asn   Ala
            75                            80

Thr   Asn   His   Ala   Ile   Leu   Gln   Ser   Leu
                  85                            90

Val   His   Leu   Met   Lys   Pro   Asn   Ala   Val
                        95

Pro   Lys   Ala   Cys   Cys   Ala   Pro   Thr   Lys
100                           105

Leu   Ser   Ala   Thr   Ser   Val   Leu   Tyr   Tyr
      110                           115

Asp   Ser   Ser   Asn   Asn   Val   Ile   Leu   Arg
            120                           125

Lys   Ala   Arg   Asn   Met   Val   Val   Lys   Ala
                  130                           135

Cys   Gly   Cys   His.
```

4.   The polypeptide chain of claim 1 wherein the
sequence comprises (Sequence ID No. 7):

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                   10

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            15                  20

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
        25                  30

Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
    35                  40
```

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
45                  50                      55

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
            60                      65

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        70                  75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        80                  85

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
    90                  95

Xaa Cys Xaa
100
```

and wherein each Xaa independently represents one of
the 20 naturally occurring L-isomer, α-amino acids,
and together with said 8 cysteine residues define
said polypeptide chain.

5.   The polypeptide chain of claim 1 wherein the
sequence comprises (Sequence ID No. 8):

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                   10

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            15                  20

Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
        25                  30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    35                  40

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
45                  50                      55

Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa
            60                      65
```

$$\text{Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa}$$
$$70 \qquad\qquad\qquad\qquad 75$$

$$\text{Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa}$$
$$80 \qquad\qquad\qquad\qquad 85$$

$$\text{Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa}$$
$$90 \qquad\qquad\qquad 95$$

wherein each Xaa independently represents one of the 20 naturally occurring L-isomer, α-amino acids, and together with said 7 cysteine residues define said polypeptide chain.

6.   A polypeptide chain useful as a subunit of a dimeric osteogenic protein, said protein being capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix;
        said polypeptide chain comprising the amino acid sequence (Sequence ID No. 5):

$$\text{Cys } Xaa_1 \; Xaa_2 \text{ His Glu Leu Tyr Val } Xaa_3 \text{ Phe}$$
$$1 \qquad\qquad\qquad 5 \qquad\qquad\qquad\qquad 10$$

$$Xaa_4 \text{ Asp Leu Gly Trp } Xaa_5 \text{ Asp Trp } Xaa_6 \text{ Ile}$$
$$15 \qquad\qquad\qquad\qquad 20$$

$$\text{Ala Pro } Xaa_7 \text{ Gly Tyr } Xaa_8 \text{ Ala Tyr Tyr Cys}$$
$$25 \qquad\qquad\qquad\qquad 30$$

$$\text{Glu Gly Cys } Xaa_9 \text{ Phe Pro Leu } Xaa_{10} \text{ Ser } Xaa_{11}$$
$$35 \qquad\qquad\qquad\qquad 40$$

$$\text{Met Asn Ala Thr Asn His Ala Ile } Xaa_{12} \text{ Thr}$$
$$45 \qquad\qquad\qquad\qquad 50$$

$$\text{Leu } Xaa_{13} \; Xaa_{14} \; Xaa_{15} \; Xaa_{16} \; Xaa_{17} \; Xaa_{18} \text{ Val}$$
$$55$$

$$\text{Pro Lys } Xaa_{19} \text{ Cys Cys Ala Pro Thr } Xaa_{20} \text{ Leu}$$
$$60 \qquad\qquad\qquad\qquad 65$$

Xaa_{21} Ala Xaa_{22} Ser Val Leu Tyr Xaa_{23} Asp
      70   75

Xaa_{24} Ser Xaa_{25} Asn Val Xaa_{26} Leu Xaa_{27} Lys
        80   85

Xaa_{28} Pro Asn Met Val Val Xaa_{29} Ala Cys Gly
        90   95

Cys His,

wherein Xaa_1 = (Lys or Arg); Xaa_2 = (Lys or Arg); Xaa_3 = (Ser or Arg); Xaa_4 = (Arg or Gln); Xaa_5 = (Gln or Leu); Xaa_6 = (Ile or Val); Xaa_7 = (Glu or Gln); Xaa_8 = (Ala or Ser); Xaa_9 = (Ala or Ser); Xaa_{10} = (Asn or Asp); Xaa_{11} = (Tyr or Cys); Xaa_{12} = (Val or Leu); Xaa_{13} = (His or Asn); Xaa_{14} = (Phe or Leu); Xaa_{15} = (Ile or Met); Xaa_{16} = (Asn or Lys); Xaa_{17} = (Glu, Asp or Asn); Xaa_{18} = (Thr, Ala or Val); Xaa_{19} = (Pro or Ala); Xaa_{20} = (Gln or Lys); Xaa_{21} = (Asn or Ser); Xaa_{22} = (Ile or Thr); Xaa_{23} = (Phe or Tyr); Xaa_{24} = (Asp, Glu or Ser); Xaa_{25} = (Ser or Asn); Xaa_{26} = (Ile or Asp); Xaa_{27} = (Lys or Arg); Xaa_{28} = (Tyr, Ala or His); and Xaa_{29} = (Arg or Lys).

7. The polypeptide chain of claim 6 wherein Xaa_{11} = Cys.

8. A polypeptide chain useful as a subunit of a dimeric osteogenic protein, said protein being capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix;

the amino acid sequence of said polypeptide chain being at least 70% homologous with the amino acid sequence (Sequence ID No. 1):

mOP-2

Ala 1	Ala	Arg	Pro	Leu 5	Lys	Arg	Arg	Gln
Pro 10	Lys	Lys	Thr	Asn	Glu 15	Leu	Pro	His
Pro	Asn 20	Lys	Leu	Pro	Gly	Ile 25	Phe	Asp
Asp	Gly	His 30	Gly	Ser	Arg	Gly	Arg 35	Glu
Val	Cys	Arg	Arg 40	His	Glu	Leu	Tyr	Val 45
Arg	Phe	Arg	Asp	Leu 50	Gly	Trp	Leu	Asp
Trp 55	Val	Ile	Ala	Pro	Gln 60	Gly	Tyr	Ser
Ala	Tyr 65	Tyr	Cys	Glu	Gly	Glu 70	Cys	Ala
Phe	Pro	Leu 75	Asp	Ser	Cys	Met	Asn 80	Ala
Thr	Asn	His	Ala 85	Ile	Leu	Gln	Ser	Leu 90
Val	His	Leu	Met	Lys 95	Pro	Asp	Val	Val
Pro 100	Lys	Ala	Cys	Cys	Ala 105	Pro	Thr	Lys
Leu	Ser 110	Ala	Thr	Ser	Val	Leu 115	Tyr	Tyr
Asp	Ser	Ser 120	Asn	Asn	Val	Ile	Leu 125	Arg
Lys	His	Arg	Asn 130	Met	Val	Val	Lys	Ala 135
Cys	Gly	Cys	His.					

9.   The polypeptide chain of claim 8 wherein the amino acid sequence is at least 80% homologous with the amino acid sequence (Sequence ID No. 1):

<u>mOP-2</u>

Ala 1	Ala	Arg	Pro	Leu 5	Lys	Arg	Arg	Gln
Pro 10	Lys	Lys	Thr	Asn	Glu 15	Leu	Pro	His
Pro	Asn 20	Lys	Leu	Pro	Gly	Ile 25	Phe	Asp
Asp	Gly	His 30	Gly	Ser	Arg	Gly	Arg 35	Glu
Val	Cys	Arg	Arg 40	His	Glu	Leu	Tyr	Val 45
Arg	Phe	Arg	Asp	Leu 50	Gly	Trp	Leu	Asp
Trp 55	Val	Ile	Ala	Pro	Gln 60	Gly	Tyr	Ser
Ala	Tyr 65	Tyr	Cys	Glu	Gly	Glu 70	Cys	Ala
Phe	Pro	Leu 75	Asp	Ser	Cys	Met	Asn 80	Ala
Thr	Asn	His	Ala 85	Ile	Leu	Gln	Ser	Leu 90
Val	His	Leu	Met	Lys 95	Pro	Asp	Val	Val
Pro 100	Lys	Ala	Cys	Cys	Ala 105	Pro	Thr	Lys
Leu	Ser 110	Ala	Thr	Ser	Val	Leu 115	Tyr	Tyr
Asp	Ser	Ser 120	Asn	Asn	Val	Ile	Leu 125	Arg

Lys His Arg Asn Met Val Val Lys Ala
                   130   135

Cys Gly Cys His.

10.   The polypeptide chain of claim 8 wherein the
amino acid sequence comprises (Sequence ID No. 1):

mOP-2

Ala Ala Arg Pro Leu Lys Arg Arg Gln
 1   5

Pro Lys Lys Thr Asn Glu Leu Pro His
 10   15

Pro Asn Lys Leu Pro Gly Ile Phe Asp
      20   25

Asp Gly His Gly Ser Arg Gly Arg Glu
           30   35

Val Cys Arg Arg His Glu Leu Tyr Val
                40   45

Arg Phe Arg Asp Leu Gly Trp Leu Asp
                50

Trp Val Ile Ala Pro Gln Gly Tyr Ser
 55   60

Ala Tyr Tyr Cys Glu Gly Glu Cys Ala
      65   70

Phe Pro Leu Asp Ser Cys Met Asn Ala
           75   80

Thr Asn His Ala Ile Leu Gln Ser Leu
                85   90

Val His Leu Met Lys Pro Asp Val Val
                     95

Pro Lys Ala Cys Cys Ala Pro Thr Lys
100   105

Leu Ser Ala Thr Ser Val Leu Tyr Tyr
    110   115

Asp Ser Ser Asn Asn Val Ile Leu Arg
        120   125

Lys His Arg Asn Met Val Val Lys Ala
            130   135

Cys Gly Cys His.

11.   The polypeptide chain of claim 8 wherein the
amino acid sequence comprises (Sequence ID No. 3):

hOP-2

Ala Val Arg Pro Leu Arg Arg Arg Gln
1   5

Pro Lys Lys Ser Asn Glu Leu Pro Gln
10   15

Ala Asn Arg Leu Pro Gly Ile Phe Asp
    20   25

Asp Val Asn Gly Ser His Gly Arg Gln
        30   35

Val Cys Arg Arg His Glu Leu Tyr Val
            40   45

Ser Phe Gln Asp Leu Gly Trp Leu Asp
                50

Trp Val Ile Ala Pro Gln Gly Tyr Ser
55   60

Ala Tyr Tyr Cys Glu Gly Glu Cys Ser
    65   70

Phe Pro Leu Asp Ser Cys Met Asn Ala
        75   80

Thr Asn His Ala Ile Leu Gln Ser Leu
            85   90

```
Val   His   Leu   Met   Lys   Pro   Asn   Ala   Val
                        95

Pro   Lys   Ala   Cys   Cys   Ala   Pro   Thr   Lys
100                           105

Leu   Ser   Ala   Thr   Ser   Val   Leu   Tyr   Tyr
      110                           115

Asp   Glu   Ser   Asn   Asn   Val   Ile   Leu   Arg
            120                           125

Lys   Ala   Arg   Asn   Met   Val   Val   Lys   Ala
                  130                           135

Cys   Gly   Cys   His.
```

12.   The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 9):

hOP-2P

```
            Pro   Leu   Arg   Arg   Arg   Gln
            1                       5

Pro   Lys   Lys   Ser   Asn   Glu   Leu   Pro   Gln
                  10                            15

Ala   Asn   Arg   Leu   Pro   Gly   Ile   Phe   Asp
                        20

Asp   Val   Asn   Gly   Ser   His   Gly   Arg   Gln
25                            30

Val   Cys   Arg   Arg   His   Glu   Leu   Tyr   Val
      35                            40

Ser   Phe   Gln   Asp   Leu   Gly   Trp   Leu   Asp
            45                            50

Tyr   Val   Ile   Ala   Pro   Gln   Gly   Tyr   Ser
                  55                            60

Ala   Tyr   Tyr   Cys   Glu   Gly   Glu   Cys   Ser
                        65
```

Phe 70	Pro	Leu	Asp	Ser	Cys 75	Met	Asn	Ala
Thr	Asn 80	His	Ala	Ile	Leu	Gln 85	Ser	Leu
Val	His	Leu 90	Met	Lys	Pro	Asn	Ala 95	Val
Pro	Lys	Ala	Cys 100	Cys	Ala	Pro	Thr	Lys 105
Leu	Ser	Ala	Thr	Ser 110	Val	Leu	Tyr	Tyr
Asp 115	Glu	Ser	Asn	Asn	Val 120	Ile	Leu	Arg
Lys	Ala 125	Arg	Asn	Met	Val	Val 130	Lys	Ala
Cys	Gly	Cys 135	His.					

13.   The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 10):

hOP-2R

						Arg 1	Arg	Gln
Pro	Lys 5	Lys	Ser	Asn	Glu	Leu 10	Pro	Gln
Ala	Asn	Arg 15	Leu	Pro	Gly	Ile	Phe 20	Asp
Asp	Val	Asn	Gly 25	Ser	His	Gly	Arg	Gln 30
Val	Cys	Arg	Arg	His 35	Glu	Leu	Tyr	Val

Ser 40	Phe	Gln	Asp	Leu	Gly 45	Trp	Leu	Asp
Tyr	Val 50	Ile	Ala	Pro	Gln	Gly 55	Tyr	Ser
Ala	Tyr	Tyr 60	Cys	Glu	Gly	Glu	Cys 65	Ser
Phe	Pro	Leu	Asp 70	Ser	Cys	Met	Asn	Ala 75
Thr	Asn	His	Ala	Ile 80	Leu	Gln	Ser	Leu
Val 85	His	Leu	Met	Lys	Pro 90	Asn	Ala	Val
Pro	Lys 95	Ala	Cys	Cys	Ala	Pro 100	Thr	Lys
Leu	Ser	Ala 105	Thr	Ser	Val	Leu	Tyr 110	Tyr
Asp	Glu	Ser	Asn 115	Asn	Val	Ile	Leu	Arg 120
Lys	Ala	Arg	Asn	Met 125	Val	Val	Lys	Ala
Cys 130	Gly	Cys	His.					

14.   The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 11):

<u>hOP-2S</u>

					Ser 1	Gln	Gln
Pro	Phe 5	Val	Val	Thr	Phe	Phe 10	Arg	Ala
Ser	Pro	Ser 15	Pro	Ile	Arg	Thr	Pro 20	Arg

Ala	Val	Arg	Pro 25	Leu	Arg	Arg	Arg	Gln 30

Ala Val Arg Pro Leu Arg Arg Arg Gln
                25   30

Pro Lys Lys Ser Asn Glu Leu Pro Gln
            35

Ala Asn Arg Leu Pro Gly Ile Phe Asp
40   45

Asp Val Asn Gly Ser His Gly Arg Gln
    50   55

Val Cys Arg Arg His Glu Leu Tyr Val
        60   65

Ser Phe Gln Asp Leu Gly Trp Leu Asp
            70   75

Tyr Val Ile Ala Pro Gln Gly Tyr Ser
                80

Ala Tyr Tyr Cys Glu Gly Glu Cys Ser
85   90

Phe Pro Leu Asp Ser Cys Met Asn Ala
    95   100

Thr Asn His Ala Ile Leu Gln Ser Leu
        105   110

Val His Leu Met Lys Pro Asn Ala Val
            115   120

Pro Lys Ala Cys Cys Ala Pro Thr Lys
                125

Leu Ser Ala Thr Ser Val Leu Tyr Tyr
130   135

Asp Glu Ser Asn Asn Val Ile Leu Arg
    140   145

Lys Ala Arg Asn Met Val Val Lys Ala
        150   165

Cys Gly Cys His.
            170

15.   A polypeptide chain useful as a subunit of a
dimeric osteogenic protein, said protein being
capable of inducing endochondral bone formation when
implanted in a mammal in association with a matrix;
         said polypeptide chain having an amino acid
sequence comprising (Sequence ID No. 2):

Prepro mOP-2

Met 1	Ala	Met	Arg	Pro 5	Gly	Pro	Leu
Trp	Leu 10	Leu	Gly	Leu	Ala	Leu 15	Cys	Ala
Leu	Gly	Gly 20	Gly	His	Gly	Pro	Gly 25	Pro
Pro	His	Thr	Cys 30	Pro	Gln	Arg	Arg	Leu 35
Gly	Ala	Arg	Asp	Arg 40	Asp	Met	Gln	Arg
Glu 45	Ile	Leu	Ala	Val	Leu 50	Gly	Leu	Pro
Gly	Arg 55	Pro	Asp	Pro	Val	His 60	Asn	Pro
Pro	Leu	Pro 65	Gly	Thr	Gln	Arg 70	Ala	Pro
Leu	Phe	Met	Leu 70	Asp	Leu	Tyr	His 80	Ala
Met	Thr	Asp	Asp	Asp 85	Asp	Gly	Gly	Pro
Pro 90	Gln	Ala	His	Leu	Gly 95	Arg	Ala	Asp
Leu	Val 100	Met	Ser	Phe	Val	Asn 105	Met	Val

Glu	Arg	Asp 110	Arg	Thr	Leu	Gly	Tyr 115	Gln
Glu	Pro	His	Trp 120	Lys	Glu	Phe	His	Phe 125
Asp	Leu	Thr	Gln	Ile 130	Pro	Ala	Gly	Glu
Ala 135	Val	Thr	Ala	Ala	Glu 140	Phe	Arg	Ile
Tyr	Lys 145	Glu	Pro	Ser	Thr	His 150	Pro	Leu
Asn	Thr	Thr 155	Leu	His	Ile	Ser	Met 160	Phe
Glu	Val	Val	Gln 165	Glu	His	Ser	Asn	Arg 170
Glu	Ser	Asp	Leu	Phe 175	Phe	Leu	Asp	Leu
Gln 180	Thr	Leu	Arg	Ser	Gly 185	Asp	Glu	Gly
Trp	Leu 190	Val	Leu	Asp	Ile	Thr 195	Ala	Ala
Ser	Asp	Arg 200	Trp	Leu	Leu	Asn	His 205	His
Lys	Asp	Leu	Gly 210	Leu	Arg	Leu	Tyr	Val 215
Glu	Thr	Ala	Asp	Gly 220	His	Ser	Met	Asp
Pro 225	Gly	Leu	Ala	Gly	Leu 230	Leu	Gly	Arg
Gln	Ala 235	Pro	Arg	Ser	Arg	Gln 240	Pro	Phe
Met	Val	Thr 245	Phe	Phe	Arg	Ala	Ser 250	Gln
Ser	Pro	Val	Arg 255	Ala	Pro	Arg	Ala	Ala 260

Arg Pro Leu Lys Arg Arg Gln Pro Lys
                    265

Lys Thr Asn Glu Leu Pro His Pro Asn
270   275

Lys Leu Pro Gly Ile Phe Asp Asp Gly
280   285

His Gly Ser Arg Gly Arg Glu Val Cys
          290   295

Arg Arg His Glu Leu Tyr Val Arg Phe
               300   305

Arg Asp Leu Gly Trp Leu Asp Trp Val
                    310

Ile Ala Pro Gln Gly Tyr Ser Ala Tyr
315   320

Tyr Cys Glu Gly Glu Cys Ala Phe Pro
     325   330

Leu Asp Ser Cys Met Asn Ala Thr Asn
          335   340

His Ala Ile Leu Gln Ser Leu Val His
               345   350

Leu Met Lys Pro Asp Val Val Pro Lys
                    355

Ala Cys Cys Ala Pro Thr Lys Leu Ser
360   365

Ala Thr Ser Val Leu Tyr Tyr Asp Ser
     370   375

Ser Asn Asn Val Ile Leu Arg Lys His
          380   385

Arg Asn Met Val Val Lys Ala Cys Gly
               390   395

Cys His.

16.   A polypeptide chain useful as a subunit of a
dimeric osteogenic protein, said protein being

capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix;

said polypeptide chain comprising the amino acid sequence (Sequence ID No. 4):

Prepro hOP-2

Met	Thr	Ala	Leu	Pro	Gly	Pro	Leu	Trp
1				5				
Leu	Leu	Gly	Leu	Ala	Leu	Cys	Ala	Leu
10					15			
Gly	Gly	Gly	Gly	Pro	Gly	Leu	Arg	Pro
	20					25		
Pro	Pro	Gly	Cys	Pro	Gln	Arg	Arg	Leu
		30					35	
Gly	Ala	Arg	Asp	Arg	Asp	Val	Gln	Arg
			40					45
Glu	Ile	Leu	Ala	Val	Leu	Gly	Leu	Pro
				50				
Gly	Arg	Pro	Arg	Pro	Arg	Ala	Pro	Pro
55					60			
Ala	Ala	Ser	Arg	Leu	Pro	Ala	Ser	Ala
	65					70		
Pro	Leu	Phe	Met	Leu	Asp	Leu	Tyr	His
		75					80	
Arg	Met	Ala	Gly	Asp	Asp	Asp	Glu	Asp
			85					90
Gly	Ala	Ala	Glu	Ala	Leu	Gly	Arg	Ala
				95				
Asp	Leu	Val	Met	Ser	Phe	Val	Asn	Met
100					105			
Val	Glu	Arg	Asp	Arg	Ala	Leu	Gly	His
	110					115		

Gln Glu Pro His Trp Lys Glu Phe Arg
         120   125

Phe Asp Leu Thr Gln Ile Pro Ala Gly
             130   135

Glu Ala Val Thr Ala Ala Glu Phe Arg
                 140

Ile Tyr Lys Val Pro Ser Ile His Leu
145   150

Leu Asn Arg Thr Leu His Val Ser Met
    155   160

Phe Gln Val Val Gln Glu Gln Ser Asn
        165   170

Arg Glu Ser Asp Leu Phe Phe Leu Asp
            175   180

Leu Gln Thr Leu Arg Ala Gly Asp Glu
                185

Gly Trp Leu Val Leu Asp Val Thr Ala
190   195

Ala Ser Asp Cys Trp Leu Leu Lys Arg
    200   205

His Lys Asp Leu Gly Leu Arg Leu Tyr
        210   215

Val Glu Thr Glu Asp Gly His Ser Val
            220   225

Asp Pro Gly Leu Ala Gly Leu Leu Gly
                230

Gln Arg Ala Pro Arg Ser Gln Gln Pro
235   240

Phe Val Val Thr Phe Phe Arg Ala Ser
    245   250

Pro Ser Pro Ile Arg Thr Pro Arg Ala
        255   260

Val	Arg	Pro	Leu 265	Arg	Arg	Arg	Gln	Pro 270
Lys	Lys	Ser	Asn	Glu 275	Leu	Pro	Gln	Ala
Asn 280	Arg	Leu	Pro	Gly	Ile 285	Phe	Asp	Asp
Val	His 290	Gly	Ser	His	Gly	Arg 295	Gln	Val
Cys	Arg	Arg 300	His	Glu	Leu	Tyr	Val 305	Ser
Phe	Gln	Asp	Leu 310	Gly	Trp	Leu	Asp	Trp 315
Val	Ile	Ala	Pro	Gln 320	Gly	Tyr	Ser	Ala
Tyr 325	Tyr	Cys	Glu	Gly	Glu 330	Cys	Ser	Phe
Pro	Leu 335	Asp	Ser	Cys	Met	Asn 340	Ala	Thr
Asn	His	Ala 345	Ile	Leu	Gln	Ser	Leu 350	Val
His	Leu	Met	Lys 355	Pro	Asn	Ala	Val	Pro 360
Lys	Ala	Cys	Cys	Ala 365	Pro	Thr	Lys	Leu
Ser 370	Ala	Thr	Ser	Val	Leu 375	Tyr	Tyr	Asp
Ser	Ser 380	Asn	Asn	Val	Ile	Leu 385	Arg	Lys
Ala	Arg	Asn 390	Met	Val	Val	Lys	Ala 395	Cys
Gly	Cys	His.						

17.   A dimeric osteogenic protein capable of
inducing endochondral bone formation in a mammal when

implanted in said mammal in association with a matrix;

said protein comprising a pair of
disulfide-bonded polypeptide chains constituting a
dimeric species, wherein each said polypeptide chain
is the polypeptide chain of claim 1, 6, 8, 15 or 16.

18.   The polypeptide chain of claim 1, 6, 8, 15
or 16 produced by expression of recombinant DNA in a
host cell.

19.   The polypeptide chain of claim 15 wherein
said host cell is a procaryotic host cell.

20.   The polypeptide chain of claim 15 wherein
said host cell is a mammalian cell.

21.   The polypeptide of claim 1, 6, 8, 15 or 16
that is glycosylated.

22.   A DNA encoding the polypeptide chain of
claim 1, 6, 8, 15 or 16.

23.   A dimeric protein comprising a pair of
polypeptide chains expressed from a DNA sequence
sufficiently duplicative of the sequence of Sequence
ID No. 2 or Sequence ID No. 4 such that, when said
polypeptide chains are oxidized to produce a
disulfide-bonded dimeric species, the dimeric species
has a conformation that is capable of inducing
endochondral bone or cartilage formation when
disposed within a matrix and implanted in a mammal.